

Leonard Lipovich

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

13,701
citations

37
h-index

79
g-index

79
ext. papers

16,023
ext. citations

8.1
avg, IF

5.64
L-index

#	Paper	IF	Citations
70	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
69	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006 , 38, 431-40	36.3	1920
68	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
67	Computational and experimental analysis of microsatellites in rice (<i>Oryza sativa</i> L.): frequency, length variation, transposon associations, and genetic marker potential. <i>Genome Research</i> , 2001 , 11, 1441-52	9.7	1103
66	An atlas of human long non-coding RNAs with accurate 5Sends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
65	Evolutionary conservation of long non-coding RNAs; sequence, structure, function. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 1063-71	4	434
64	Prolonged myelination in human neocortical evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16480-5	11.5	355
63	Whole-genome cartography of estrogen receptor alpha binding sites. <i>PLoS Genetics</i> , 2007 , 3, e87	6	352
62	Metabolic costs and evolutionary implications of human brain development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13010-5	11.5	298
61	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010 , 16, 1478-87	5.8	295
60	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012 , 22, 1646-57	9.7	292
59	Conserved long noncoding RNAs transcriptionally regulated by Oct4 and Nanog modulate pluripotency in mouse embryonic stem cells. <i>Rna</i> , 2010 , 16, 324-37	5.8	257
58	Complex Loci in human and mouse genomes. <i>PLoS Genetics</i> , 2006 , 2, e47	6	246
57	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005 , 2, 105-11	21.6	218
56	MacroRNA underdogs in a microRNA world: evolutionary, regulatory, and biomedical significance of mammalian long non-protein-coding RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010 , 1799, 597-615	6	179
55	Sall4 regulates distinct transcription circuitries in different blastocyst-derived stem cell lineages. <i>Cell Stem Cell</i> , 2008 , 3, 543-54	18	171
54	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017 , 14, e1002215	11.6	162

53	REST regulates distinct transcriptional networks in embryonic and neural stem cells. <i>PLoS Biology</i> , 2008 , 6, e256	9.7	155
52	Genome-wide mapping of RELA(p65) binding identifies E2F1 as a transcriptional activator recruited by NF-kappaB upon TLR4 activation. <i>Molecular Cell</i> , 2007 , 27, 622-35	17.6	149
51	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147
50	Activity-dependent human brain coding/noncoding gene regulatory networks. <i>Genetics</i> , 2012 , 192, 1133-48	14.8	135
49	Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. <i>Journal of Neurochemistry</i> , 2011 , 116, 459-66	6	134
48	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. <i>Journal of Perinatal Medicine</i> , 2010 , 38, 617-43	2.7	111
47	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017 , 120, 341-353	15.7	97
46	5S Long serial analysis of gene expression (LongSAGE) and 3S LongSAGE for transcriptome characterization and genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11701-6	11.5	90
45	Synaptogenesis and development of pyramidal neuron dendritic morphology in the chimpanzee neocortex resembles humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110 Suppl 2, 10395-401	11.5	88
44	Pseudogene-derived lncRNAs: emerging regulators of gene expression. <i>Frontiers in Genetics</i> , 2014 , 5, 476	4.5	86
43	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009 , 15, 85-96	5.8	79
42	Mice and men: their promoter properties. <i>PLoS Genetics</i> , 2006 , 2, e54	6	75
41	Phylogenomic analyses reveal convergent patterns of adaptive evolution in elephant and human ancestries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20824-9	11.5	63
40	Promoter analysis reveals globally differential regulation of human long non-coding RNA and protein-coding genes. <i>PLoS ONE</i> , 2014 , 9, e109443	3.7	62
39	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017 , 7, 40127	4.9	59
38	Global discovery of primate-specific genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 12019-24	11.5	58
37	Developmental changes in the transcriptome of human cerebral cortex tissue: long noncoding RNA transcripts. <i>Cerebral Cortex</i> , 2014 , 24, 1451-9	5.1	55
36	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322	9.7	54

35	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016 , 99, 56-75	11	41
34	Making sense of Dlx1 antisense RNA. <i>Developmental Biology</i> , 2013 , 376, 224-35	3.1	37
33	Sense-antisense gene pairs: sequence, transcription, and structure are not conserved between human and mouse. <i>Frontiers in Genetics</i> , 2013 , 4, 183	4.5	36
32	The Growth-Arrest-Specific (-)5 Long Non-Coding RNA: A Fascinating lncRNA Widely Expressed in Cancers. <i>Non-coding RNA</i> , 2019 , 5,	7.1	34
31	Identification of long noncoding RNAs dysregulated in the midbrain of human cocaine abusers. <i>Journal of Neurochemistry</i> , 2015 , 135, 50-9	6	31
30	Dynamic gene expression in the human cerebral cortex distinguishes children from adults. <i>PLoS ONE</i> , 2012 , 7, e37714	3.7	27
29	Transcriptome interrogation of human myometrium identifies differentially expressed sense-antisense pairs of protein-coding and long non-coding RNA genes in spontaneous labor at term. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2014 , 27, 1397-408	2	21
28	Global Intersection of Long Non-Coding RNAs with Processed and Unprocessed Pseudogenes in the Human Genome. <i>Frontiers in Genetics</i> , 2016 , 7, 26	4.5	21
27	miRCOVID-19: Potential Targets of Human miRNAs in SARS-CoV-2 for RNA-Based Drug Discovery. <i>Non-coding RNA</i> , 2021 , 7,	7.1	19
26	Genomic structure and evolutionary context of the human feline leukemia virus subgroup C receptor (hFLVCR) gene: evidence for block duplications and de novo gene formation within duplicons of the hFLVCR locus. <i>Gene</i> , 2002 , 286, 203-13	3.8	18
25	Quality assessment of the Affymetrix U133A&B probesets by target sequence mapping and expression data analysis. <i>In Silico Biology</i> , 2007 , 7, 241-60	2	18
24	Primate-specific endogenous cis-antisense transcription in the human 5q31 protocadherin gene cluster. <i>Journal of Molecular Evolution</i> , 2006 , 62, 73-88	3.1	14
23	Detailed characterization of the mouse embryonic stem cell transcriptome reveals novel genes and intergenic splicing associated with pluripotency. <i>BMC Genomics</i> , 2008 , 9, 155	4.5	12
22	FuncPEP: A Database of Functional Peptides Encoded by Non-Coding RNAs. <i>Non-coding RNA</i> , 2020 , 6,	7.1	10
21	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016 , 6, 28199	4.9	9
20	On-the-Fly Integration and Ad Hoc Querying of Life Sciences Databases Using LifeDB. <i>Lecture Notes in Computer Science</i> , 2009 , 561-575	0.9	9
19	Anti-centrosome antibodies in breast cancer are the expression of autoimmunity. <i>Immunologic Research</i> , 2014 , 60, 339-47	4.3	8
18	Tissue-restricted transcription from a conserved intragenic CpG island in the Klf1 gene in mice. <i>Biology of Reproduction</i> , 2012 , 87, 108	3.9	8

17	Abundant novel transcriptional units and unconventional gene pairs on human chromosome 22. <i>Genome Research</i> , 2006 , 16, 45-54	9.7	8
16	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014 , 15, 1177	4.5	7
15	Primate-specific oestrogen-responsive long non-coding RNAs regulate proliferation and viability of human breast cancer cells. <i>Open Biology</i> , 2016 , 6,	7	7
14	Characterization of human cortical gene expression in relation to glucose utilization. <i>American Journal of Human Biology</i> , 2013 , 25, 418-30	2.7	6
13	A Long Non-coding RNA, , Is an Effector Transcript at the Chromosome 8p23.1- Metabolic Traits and Type 2 Diabetes Risk Locus. <i>Frontiers in Genetics</i> , 2020 , 11, 615	4.5	5
12	Association of the IGF1 gene with fasting insulin levels. <i>European Journal of Human Genetics</i> , 2016 , 24, 1337-43	5.3	4
11	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
10	YY1 directly interacts with myocardin to repress the triad myocardin/SRF/CArG box-mediated smooth muscle gene transcription during smooth muscle phenotypic modulation. <i>Scientific Reports</i> , 2020 , 10, 21781	4.9	4
9	Unintended target effect of anti-BCL-2 DNAi. <i>Cancer Management and Research</i> , 2017 , 9, 427-432	3.6	3
8	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2019 , 19, 97-108	3.5	3
7	Challenging paradigms: long non-coding RNAs in breast ductal carcinoma in situ (DCIS). <i>Frontiers in Genetics</i> , 2013 , 4, 50	4.5	2
6	High-throughput RNA sequencing reveals structural differences of orthologous brain-expressed genes between western lowland gorillas and humans. <i>Journal of Comparative Neurology</i> , 2016 , 524, 288-308	3.4	2
5	Reply to Skoyles: Decline in growth rate, not muscle mass, predicts the human childhood peak in brain metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4910	11.5	1
4	Structural differences of orthologous genes: insights from human-primate comparisons. <i>Genomics</i> , 2008 , 92, 134-43	4.3	1
3	Dietary Patterns and Associated Microbiome Changes that Promote Oncogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 725821	5.7	1
2	Gestational Age Dependence of the Maternal Circulating Long Non-Coding RNA Transcriptome During Normal Pregnancy Highlights Antisense and Pseudogene Transcripts. <i>Frontiers in Genetics</i> , 2021 , 12, 760849	4.5	1
1	A collective statement in support of saving pangolins.. <i>Science of the Total Environment</i> , 2022 , 153666	10.2	0